RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/409, 800A_

Source: _1645_

Date Processed by STIC: _4/25/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

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<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ✓ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of **n's** or **Xaa's** (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of **"Artificial"** (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Blattner, Frederick R.

Burland, Valerie
Rose, Debra J.
Mayhew, George F.
Perna, Nicole
Perry, Robert D.
Straley, Susan C.
Fetherston, Jacqueline D.
Lindler, Luther E.
Plano, Gregory V.

[handwritten: move over / (global enur) do not show these numbers]

[handwritten: Do NOT use TAB codes. They do not process well in the CRF program,]

(ii) TITLE OF INVENTION: Plasmid DNA from Yersinia Pestis

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

    (A) ADDRESSEE: Quarles & Brady
    (B) STREET: 1 South Pinckney Street
    (C) CITY: Madison
    (D) STATE: WI
    (E) COUNTRY: US
    (F) ZIP: 53701-2113

[handwritten: move over]

(v) COMPUTER READABLE FORM:

    (A) MEDIUM TYPE: Floppy disk
    (B) COMPUTER: IBM PC compatible
    (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    (D) SOFTWARE: Word Perfect 8.0

(vi) CURRENT APPLICATION DATA:

    (A) APPLICATION NUMBER: 09/409,800
    (B) FILING DATE: 09/30/99
    (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

    (A) NAME: Seay, Nicholas J.
    (B) REGISTRATION NUMBER: 27386
    (C) REFERENCE/DOCKET NUMBER: 960296.95939

(ix) TELECOMMUNICATION INFORMATION:

    (A) TELEPHONE: (608) 251-5000
    (B) TELEFAX: (608) 251-9166

(2) INFORMATION FOR SEQ ID NO: 1

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 100990
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: circular

use upper-case letters for bases when creating Sequence Listing in "old" sequence Rules format

      (ii) MOLECULE TYPE: DNA   (plasmid) *insert ↓*

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: ↓

```
(10)  aaacagcccg gcgtgctgga gcgactggaa cgtgaggacg gtgtcattat ccaccagcgt 60

      cgcgagtggc gcatgtacga tccggaaaca ggtaagctca cgacgaaggc cggaacgctc 120

      tggggtctgc tgaagaaaat ccactgataa caccaaccac tgcggtgagt agccagctca 180

      ccgcgcgcgt atctgggtca taaccactgt agtgagtaaa acggctgccg tggcatccgg 240

      tatccactgt agtgagtaaa gtggtgatta tcgacttcac tatccactgt agagagtaaa 300

(15)  caggcgttca ttcacagcaa acaaccacta tggagagtga tggaatgcga cctccagcgg 360

      gtatccacta tggagagtaa accttcactg ttttcagcgg atgtctactc tccacagtgg 420

      atagtaaatc cagccaaccg attctgctct ccatagtgga tagccaatag cgaagggagc 480

      aacgataacc actatagaga gtggatttaa caagtcaccc agtgaccact aacctcgcag 540

      cccttgtttc atctaggttt gtaaccacta acattcattt cgttatttga gcgctactgc 600

(20)  ctacagtggt tactattcgg ttgttgttac tcactacagt ggatagcgga cttcagataa 660

      acaaaaggcc cactacagcg gaatagtgag cctttctact ctctacagtg attgggctat 720

      ttgcgagcct ttgccttgcg cagctcttcg agaatcgcca gttcttcctt gctcaacatg 780

      accatctcac cgtctttttc ttcaggaaca acatcgatga tgtcctcctg accatcgcca 840

      ggcaagttat cttcctgctc ttctggttct tccggcgcag ctttagttgg tggcaatgcc 900

(25)  gggcgtaact tcggccgcct atagtggatg atgaagtaga ccgagctgcc gcgcttcact 960

      tcggtgtaat cgagatagcc gatctcccgc agctgctcca tcgccttcct gactgtcgcg 1020

      ttctgggtaa tggtgcggct ggttaagtta agtctggcgc gtaagcgagc caacgagatt 1080

      ggtgccgggt caggtggcaa actttcgatg aatgtgtaga gtgcctgggc ggattctttt 1140

      ctggagagtt cgttgattgc ccggagttgc agaagaacct ttttgtcgaa ctggtagagt 1200

      tcgaaaatct taggatcagc ctgcagcgag accgtgtcgt tcttagtgct gtactttgct 1260

      gtctgcacaa ggtgagttac gtaatactca tcagagcctt tactgcggaa tgagatagtg 1320
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lines exceed ↓ 72-character limit